

SEQUENCE LISTING

SEQUENCE ID NO: 1

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SEQUENCE ID NO: 2

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SEQUENCE ID NO: 5, PCR primer

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SEQUENCE ID NO: 6, PCR primer

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SEQUENCE ID NO: 7, PCR primer

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SEQUENCE ID NO: 8, PCR primer

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SEQUENCE ID NO: 9, murine Socs2 locus

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DEFINITION Mus musculus Cish2 gene, complete sequence.  
ACCESSION AF292933  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  
Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Mus.  
REFERENCE 1 (bases 1 to 13908)  
AUTHORS Horvat,S. and Medrano,J.F.  
TITLE A 500-kb YAC and BAC contig encompassing the high-growth  
deletion  
in mouse chromosome 10 and identification of the murine  
Raidd/Cradd  
gene in the candidate region  
JOURNAL Genomics 54 (1), 159-164 (1998)  
MEDLINE 99026139  
PUBMED 9806843  
REFERENCE 2 (bases 1 to 13908)  
AUTHORS Horvat,S. and Medrano,J.F.  
TITLE Lack of expression of Socs2 causes the high growth phenotype in  
mice  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 13908)  
AUTHORS Wong,M.L. and Medrano,J.F.  
TITLE Direct Submission  
JOURNAL Submitted (01-AUG-2000) Department of Animal Science,  
University of California, Davis, One Shields Avenue, Davis, CA 95616, USA  
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13861 cagatttgc ccagatttgt tccagattaa tttggagctc tgggtctg //
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SEQUENCE ID NO: 10, exon 2 probe

4501 AGTGTCTGCG AGAGACTTTG CCACACCATT CTGCCGGAAT TTGGAGAAAA AGAACCCAGCC  
4561 GCTTCCAGTC CCCTCCCCCT CCGCCACCCT TTCGGACACC CTGCACACTC TCGTTTGGG  
4621 GTACCCTGTG ACTTCCAGG

SEQUENCE ID NO: 11, exon 3 probe

6929	CTCGCCATTA	ACAAATGTAC	CGGTACGATC	TGGGGACTGC	CTTTACCAAC	AAGACTAAAAA
6989	GATTACTTGG	AAGAATATAA	ATTCCAGGTA	TAAGTATTTC	TCTCTCTTT	TCGTTTTTTT
7049	TTAAAAAAAAA	AAAAAACACA	TGCCTCATAT	AGACTATCTC	CGAATGCAGC	TAT

SEQUENCE ID NO: 12, 3' Socs2 probe

11185	GGAATTCAAG	TCTACTTCAA	TTAGGTAAAC	TGACAGATTT	AGGGTCCTTA	GGATTAAGTC
11245	TGTGTCTGTT	TCTCTTAGT	TCTCTTCAGG	ATTTAAAAAC	CAAAGCCAGT	TCCCTAACACC
11305	ACATTTCAAC	ACTTTAAAAA	AAAAAAAAAA	AAAAAAAACCTT	GTTTATTAA	ACAACCGTAG
11365	GCTCCTTACT	TGCTAGTTA	TGCTCTATTG	GGAGGAAGA	AAGACAGCCC	TTCTTAGCT
11425	TGTTTGTGTC	TGAGGGCAAT	CCTTGCACCT	TCGGTTGGT	CTTCTCATTC	TCTCTGCTG
11485	CCCTGGAAAGA	TTTTCTCCAG	TTTTCCCTCT	ATGTGGTTTC	AGAGTAAGTC	ACCTTACCTC
11545	GCACTCAGCT	TAAGGGACAG	CTGTTGTTGG	AGTCAGCCTC	AAAAGCCCC	GTTTGTCCCCA
11605	AATGCCTGAC	TAGCGGGTCA	GCTGAAGCAG	TCATTGTGGT	CTTCCTACCC	ACCCTGTCCT
11665	CAGCTCTGTC	CACAAGGGAG	GTCTGAGCTG	CCAAGTCTGA	CGGGGGACTC	ACTCCATAAA
11725	ACATTTACTG	AGCCATAAAA	ATAAAACCTGC	TTTTATAGAC	AACTCTCACT	TTGAACTCCA
11785	TTCTTCACCT	GGAGAAGAAG	GCGCTGCC			

SEQUENCE ID NO: 13, HG deletion breakpoint 5' primer

5' -CTGGGCTCATTGGAAATG-3'

SEQUENCE ID NO: 14, HG deletion breakpoint 3' primer (I)

5' -TATTTCTCCCAATAGCTCG-3'

SEQUENCE ID NO: 15, HG deletion breakpoint 3' primer (II)

5' -CTGGCTTCTGAAAACCTTACC-3'

SEQUENCE ID NO: 16, HG deletion breakpoint 3' primer (III)

5' -GTAGATCTTGGGAGAGGAGA-3'

SEQUENCE ID NO: 17, HG deletion breakpoint 3' primer (IV)

5' -TGGGCTTCCTGGGAAAGTT-3'

SEQUENCE ID NO: 18, HG deletion breakpoint 3' primer (V)

5'-AGCTGTCGGCTGAAACGGAG-3'

SEQUENCE ID NO: 19, HG deletion breakpoint 3' primer (VI)

5'-AACGAAGTATCTTGAGTTAC-3'

SEQUENCE ID NO: 20, Merged Consensus genomic sequences of the high growth deletion in mouse chromosome 10.

The sequence covers a region of approximately 659,000 nucleotide bases of genomic DNA. Six BAC clones from the CITB mouse-BAC library corresponding to the minimal path of the physical map of the HG region (Horvat and Medrano, Genomics 54:159-164, 1998) were sequenced. The 6 BACs are: B520, B308, B546, B11I10, B9L14 and B405 and are assembled consecutively in 13 contigs. The contigs have been ordered and separated by sets of 20 Xs that identify gaps in the sequence.

The approximate location of the hg deletion is from nucleotide position 63,724 to 533,100. The breakpoint of the deletion is in position 63,724 occurred in intron-2 of the mouse *Socs2/Cish2* gene (Accession # AF292933). The deletion of exon 3 of this gene eliminates the expression of this gene in hg mice and appears to be the causative reason of the high growth phenotype.

The deletion breakpoint at position 533,100 was determined because after this position is the sequence of the *Vespr* (viral encoded semaphorin receptor) gene (mRNA seq. Accession # AF190578), which is fully expressed in hg.

The deletion encompasses the full-length sequence of the RAIDD/CRADD gene (Accession # AJ224738) (from nt 146,837 to 298,188).

DEFINITION test, 659158 bases

ORIGIN

1	CTTGATGGAG	TCGGTTGGGG	TTTTTTGTTT	GTTTGTGTTG	TTGTTTTCTG
51	GAAAGTTGAT	AAACTTAATG	AGGACATGGC	TTGCAGCGTG	GCAGGCACAA
101	CACCTGATGC	TAAGGTCCTG	ACTAATTCA	TGCTCAGAGG	TATTATTCC
151	AGTAACAGGA	GCCAATTCCA	CGTGCAGT	TGTTTACAGC	ACTGTGCTAT
201	CACAGAGGCG	CATGCGCAGT	TTGGAGGGAA	GTGTCCGGTT	GCTGTTCCCT
251	TGCTGTGTAT	TGGCTGGGGT	AAGCACCATG	GCTTCAGGT	CTGTTAAGAG
301	TGACCCAAGC	GCATGAGCAT	TGGAGACAGC	AGTGCCCGAG	CTGTTGTCAGT
351	GTTGAAACCA	GACTACAACG	CAGGAGAAAG	GACTCTGAAG	TCGACATTG
401	CTCTAGCTGT	CAAGATGATA	AAAAAATAAG	ACAATAGATG	TTGGTAAACT
451	GTCAGCTGAA	GAAGTAGAAA	TGGCCACCCCT	AAGGAGAGAA	TGGAATGCC
501	GTGAGCATGG	TCCTCAGGCA	AAGGAAGTGG	AACAGTTGAC	CAAAACCAA
551	GAAGAGGTAG	AAGGGAAATC	TCAGCAGGAG	AAGGAGAGGG	AATGGAAAGG
601	AGAAAATAGAC	AAAATCGTGG	ATTTTATAAC	TCCCGAGAGG	CACCAATTCT
651	GTTAGAAGCC	GTCCTGGCCT	TTCACTCCGG	AAAGGTTTC	TTGTTTTTC
701	TTTTTAAGT	TGCCCATCAG	GGAATTAGGC	CATTAATACT	GAATCGGATC
751	CTTGTCTGTC	CAGTTGGGTG	CTTTATTGTA	ATGATGGACA	TCTTTATAAA
801	CATCTTAATC	TTAATACATA	ACTTTTGGA	ATAAAAACCTA	GACTGACAAA
851	AACAGAATAG	TGAACAAAAG	AGAAGAAGGT	TAGCAATAAT	TGACAGTAAT
901	GTGAACCTCT	TGCCCAATGG	GAGCACTTAG	GTTCTCTCTC	TTTTTTTTAT
951	TGCATCAAAG	AAAGTAAGTC	TGATACAAGC	TTGTCAGATA	TACCAACTTT
1001	GCTCCTAACT	TTAAAAACACT	ATTAGTCTTT	TTCAAATTAA	TACCGAACAA
1051	AGCTATTAT	TTGACGGACA	AGTTGTATAT	TGACTTATCT	GAACAAGCTA
1101	TTTCTATTGA	AAAAAATTAT	ATTGACTTAT	AATAAAAGTT	TTACAAGATC
1151	AAGATAAGTT	ATGAGCATGA	AAGAACAAAGG	CTTGTAAAGTA	AAATTAAATA
1201	ATTAAAAAGT	GTTCCTGTGA	GTCCAGAGTT	GACCAATGTG	GAACCTCTAGA

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 1351 TTTGTTTGT TTTGTTTTT TTTTCGAGA CAGGGTTTCT CTGTGTAGCC  
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 75001 ACTGAGGGAT ACGAAGCCTG GGCCAATGGG AGTGCTGGAT AATGCCTCTA  
 75051 AATCTGTAGG TGTTAACCCA TGCAGTCAGG CAACATAAGT AAAAGATATT  
 75101 TTTAGAAGGC TGTGATGTTG TGACCACACA CAGGTAGTCT CCCTCATG  
 75151 CTCCCAGTCA GTGTAACAGG TGTTGGTAT AAACGTCGTT TTAGTTACTT  
 75201 ATCGATACTC AAATCACCCC CCCCCCCCCG GGCAGCGCATG CGCATGCGCA  
 75251 AGCTCAGCCT GGTATTTAA TATGGCCTTA AACAGGTGCA AGGGTCTGGG  
 75301 GCCACTCTCA AATTCCACA TGGGCTAACG CCCTCCCCCG ATACTCCTGA  
 75351 ATTATTACTT ACTAAAAATCT AAATTCCATC TTGCTACCTT AGACCCAAAT  
 75401 GAGGGACCCCT GGGTCGGCTC TTCCCAGGTT TTTCTGGCGT ATGCTCCGCT  
 75451 TCTCCAGCTC TCAGGCCTGA TTTTCTGTGTT TCCCTGGCAA AGGATTCTAA  
 75501 ATCTGTCTCTT TTCCCTGGGT TCCCTGGCC ATGAAATCTA AAGTCCCACC  
 75551 TCCGTCTCCT GCCTAGCCAT TAGCCACCTG CAACTTTATT TTCCAATTAG  
 75601 AGCCAACGGG GGCAGGGACC CGAGGCATCT TCATCTTACA TGTAGTCGTG